In the Claims:

Please cancel claims 1-33. Please add new claims 34-77. The claims and their status are shown below.

1-33. (Canceled)

34. (New) A method for characterizing an analyte (10) contained in a first fluid, comprising the steps of:

contacting the analyte (10) with a first probe (20) and a second probe (22) under conditions in which the first and second probe bind to the analyte, wherein the first probe binds specifically to at least one first binding site (12) of the analyte (10);

labeling the first and second probes with a first and a second electro-chemical label, respectively, if the first and second probes are not already electro-chemically reactive;

abstracting the first and second probes bound to the analyte;

detecting a first electro-chemical signal (Si1) caused by the first-labeled probe (20) and a second electro-chemical signal (Si2) caused by the second-labeled probe (22); and

determining the ratio between the first (Si1) and the second signal (Si2), thereby characterizing the analyte (10).

35. (New) A method for characterizing an analyte (10) contained in a first fluid, comprising the steps of:

contacting an analyte (10) with a first probe (20) under conditions in which the first probe binds to the analyte, wherein the first probe binds specifically to at least one first binding site (12) of the analyte (10);

labeling the first probe and the analyte with a first electro-chemical label and an analyte electro-chemical label, respectively, if the first probe and analyte are not already electro-chemically reactive;

abstracting the analyte bound by the first probe and the first probe bound to the analyte;

detecting a first electro-chemical signal (Si1) caused by the first-labeled probe (20) and an analyte electro-chemical signal (SiA) caused by the labeled analyte (10); and

determining the ratio between the first (Si1) and the analyte signal (SiA), thereby characterizing the analyte (10).

36. (New) The method of claim 34 or 35, wherein an electrode (27) used for the detection is not brought into contact with the first fluid.

37. (New) The method of claim 34 or 35, wherein the analyte (10) is separated from the first fluid and is transferred to a second fluid.

38. (New) The method of claim 34 or 35, wherein the analyte (10) is bound by a catcher molecule (pT, $(T)_n$).

39. (New) The method of claim 38, wherein the catcher molecule (pT, $(T)_n$) is immobilized on a first (16) or second surface.

40. (New) The method of claim 38, wherein the catcher molecule (pT, $(T)_n$) is a nucleic acid, an analogue of a nucleic acid, a peptide nucleic acid (PNA), an antibody, or a receptor.

41. (New) The method of claim 38, wherein the catcher molecule (pT, $(T)_n$) comprises an affinity molecule.

42. (New) The method of claim 34, wherein the first (20) or second probe (22) contains an affinity molecule.

43. (New) The method of claim 35, wherein the first (20) probe or the analyte (10) contains an affinity molecule.

44. (New) The method of claim 42 or 43, wherein the affinity molecule is biotin, avidin, or streptavidin.

45. (New) The method of claim 34 or 35, wherein the analyte (10) is a nucleic acid.

46. (New) The method of claim 45, wherein the nucleic acid has a poly-T-end (pT, $(T)_n$) or a poly-A-end (pA, $(A)_n$).

47. (New) The method of claim 34 or 35, wherein characterizing is determining the length or size of the analyte (10).

48. (New) The method of claim 34 or 35, wherein the analyte (10) is amplified by PCR prior to step a).

49. (New) The method of claim 34 or 35, wherein the analyte (10) is immobilized on a first (16) or second surface.

50. (New) The method of claim 49, wherein the first surface (16) is the surface of a superparamagnetic particle (18).

51. (New) The method of claim 50, wherein the particle (18) has a diameter of 10 nm to 100 μm.

52. (New) The method of claim 50, wherein the particle (18) has a diameter of 1 – 10 μm.

53. (New) The method of claim 49, wherein the second surface is an electrode (27) used for detection.

54. (New) The method of claim 53, wherein the electrode contains an electrically conductive plastic, an electrically conductive polymer, mercury, amalgam, gold, platinum, carbon, or indium tin oxide.

55. (New) The method of claim 34, wherein the second probe (22) binds specifically to at least one second binding site (14) of the analyte (10).

56. (New) The method of claim 55, wherein the analyte (10) has a known number of first binding sites (12) and an unknown number of second binding sites (14).

57. (New) The method of claim 34 or 35, wherein the analyte (10) is a DNA fragment that exhibits repetitive sequences.

58. (New) The method of claim 57, wherein the second probe binds to the repetitive sequences and the first probe does not bind to the repetitive sequences.

59. (New) The method of claim 57, wherein the repetitive sequences are a consequence of a triplet expansion disease.

60. (New) The method of claim 57, wherein the triplet expansion disease is fragile X syndrome, Huntington's disease, bulbar muscular atrophy, type I spinocerebral ataxia, myotonic dystrophy, or Friedreich's ataxia.

61. (New) The method of claim 49, wherein the first probe (20) is released from the analyte (10) and/or the analyte (10) is released from the first (16) or second surface via heat denaturation, chemical denaturation, enzymatic digestion, or chemical breakdown.

62. (New) The method of claim 34, wherein the first (20) and the second probe (22) are released separately from one another and from the analyte (10) prior to detection.

63. (New) The method of claim 49, wherein the first probe (20) is released from the analyte (10) and the analyte (10) is released from the first (16) or second surface prior to detection.

64. (New) The method of claim 34, wherein the first label (24) and/or the second label (26) are released from the first (20) and/or second probe (22) prior to detection.

65. (New) The method of claim 35, wherein the first label (24) and/or the analyte label (26) are released from the first probe (20) and/or the analyte (10) prior to detection.

66. (New) The method of claim 34 or 35, wherein the first (24) and/or the second label (26) are released by enzymatic digestion or chemical breakdown.

67. (New) The method of claim 34, wherein the first (20) and/or second probe (22) binds sequence-specifically to the analyte (10) via hybridization.

68. (New) The method of claim 34, wherein the first (20) and/or second probe (22) is a nucleic acid, an analogue of a nucleic acid, or a peptide nucleic acid (PNA).

69. (New) The method of claim 34 or 35, wherein the first signal (Si1), second signal (Si2), or analyte signal (SiA) is caused by a catalytic hydrogen release.

70. (New) The method of claim 34 or 35, wherein the labels can be reversibly reduced or oxidized.

71. (New) The method of claim 34 or 35, wherein the labels comprise an osmium complex, a nano gold particle, a cysteine, a ferrocenyle, a daunomycin, a benzoquinone, a naphthoquinone, an anthraquinone or a p-aminophenol group, or a dye.

72. (New) The method of claim 71, wherein the dye is indophenol, thiazine, or phenazine.

73. (New) The method of claim 34, wherein the first (20) or second probe (22) is labeled with multiple labels (24, 26).

74. (New) The method of claim 34, wherein the first (20) or second probe (22) has a linear primary structure on whose one end the label (24, 26) is located.

75. (New) The method of claim 34 or 35, wherein the detection of the first (Si1) and the second signal (Si2) takes place on the same electrode.

76. (New) The method of claim 34 or 35, wherein the detection takes place by means of cathodic stripping voltammetry (CSV), squarewave voltammetry, cyclic voltammetry, or chronopotentiometry.

77. (New) The method of claim 34 or 35, wherein the detection takes place by means of a reversible redox process or a catalytic hydrogen development.